


```
   1 CCGCGCCGCC GTTTGGGCCG GGWAGCGATG TAGTAGCTGC CAGGCTGTCC
  51 CCCGCCCTGC CCGGCCCGAG CCCCGCGGGC CGCCGCCGCC ACCGCCGCCA
 101 TGAAGAAGCA GTTCAACCGC ATGAAGCAGC TGGCTAACCA GACCGTGGGC
 151 AGAGCTGAGA AAACAGAAGT CCTTAGTGAA GATCTATTAC AGATTGAGAG
 201 ACGCCTGGAC ACGGTGCGGT CAATATGCCA CCATTCCCAT AAGCGCTTGG
 251 TGGCATGTTT CCAGGGCCAG CATGGCACCG ATGCCGAGAG GAGACACAAA
 301 AAACTGCCTC TGACAGCTCT TGCTCAAAAT ATGCAAGAAG CATCGACTCA
 351 GCTGGAAGAC TCTCTCCTGG GGAAGATGCT GGAGACGTGT GGAGATGCTG
 401 AGAATCAGCT GGCTCTCGAG CTCTCCCAGC ACGAAGTCTT TGTTGAGAAG
 451 GAGATCGTGG ACCCTCTGTA CGGCATAGCT GAGGTGGAGA TTCCCAACAT
 501 CCAGAAGCAG AGGAAGCAGC TTGCAAGATT GGTGTTAGAC TGGGATTCAG
 551 TCAGAGCCAG GTGGAACCAA GCTCACAAAT CCTCAGGAAC CAACTTTCAG
 601 GGGCTTCCAT CAAAAATAGA TACTCTAAAG GAAGAGATGG ATGAAGCTGG
 651 AAATAAAGTA GAACAGTGCA AGGATCAACT TGCAGCAGAC ATGTACAACT
 701 TTATGGCCAA AGAAGGGGAG TATGGCAAAT TCTTTGTTAC GTTATTAGAA
 751 GCCCAAGCAG ATTACCATAG AAAAGCATTA GCAGTCTTAG AAAAGACCCT
 801 CCCCGAAATG CGAGCCCATC AAGATAAGTG GGCGGAAAAA CCAGCCTTTG
 851 GGACTCCCCT AGCAGAACAC CTGAAGAGGA GCGGGCGCGA GATTGCGCTG
 901 CCCATTGAAG CCTGTGTCAT GCTGCTTCTG GAGACAGGCA TGAAGGAGGA
 951 GGGCCTTTTC CGAATTGGGG CTGGGGCCTC CAAGTTAAAG AAGCTGAAAG
1001 CTGCTTTGGA CTGTTCTACT TCTCACCTGG ATGAGTTCTA TTCAGACCCC
1051 CATGCTGTAG CAGGTGCTTT AAAATCCTAT TTACGGGAAT TGCCTGAACC
1101 TTTGATGACT TTTAATCTGT ATGAAGAATG GACACAAGTT GCAAGTGTGC
1151 AGGATCAAGA CAAAAAACTT CAAGACTTGT GGAGAACATG TCAGAAGTTG
1201 CCACCACAAA ATTTTGTTAA CTTTAGATAT TTGATCAAGT TCCTTGCAAA
1251 GCTTGCTCAG ACCAGCGATG TGAATAAAAT GACTCCCAGC AACATTGCGA
1301 TTGTGTTAGG CCCTAACTTG TTATGGGCCA GAAATGAAGG GACACTTGCT
1351 GAAATGGCAG CAGCCACATC CGTCCATGTG GTTGCAGTGA TTGAACCCAT
1401 CATTCAGCAT GCCGACTGGT TCTTCCCTGA AGAGGTGGAA TTTAATGTAT
1451 CAGAAGCATT TGTACCTCTC ACCACCCCGA GTTCTAATCA CTCATTCCAC
1501 ACTGGAAACG ACTCTGACTC GGGGACCCTG GAGAGGAAGC GGCCTGCTAG
1551 CATGGCGGTG ATGGAAGGAG ACTTGGTGAA GAAGGAAAGT CCTCCCAAAC
1601 CGAAGGACCC TGTATCTGCA GCTGTGCCAG CACCAGGGAG AAACAACAGT
1651 CAGATAGCAT CTGGCCAAAA TCAGCCCCAG GCAGCTGCTG GCTCCCACCA
1701 GCTCTCCATG GGCCAACCTC ACAATGCTGC AGGGCCCAGC CCGCATACAC
1751 TGCGCCGAGC TGTTAAAAAA CCCGCTCCAG CACCCCCGAA ACCGGGCAAC
1801 CCACCTCCTG GCCACCCCGG GGGCCAGAGT TCTTCAGGAA CATCTCAGCA
1851 TCCACCCAGT CTGTCACCAA AGCCACCCAC CCGAAGCCCC TCTCCTCCCA
1901 CCCAGCACAC GGGCCAGCCT CCAGGCCAGC CCTCCGCCCC CTCCCAGCTC
1951 TCAGCACCCC GGAGGTACTC CAGCAGCTTG TCTCCAATCC AAGCTCCCAA
2001 TCACCCACCG CCGCAGCCCC CTACGCAGGC CACGCCACTG ATGCACACCA
2051 AACCCAATAG CCAGGGCCCT CCCAACCCCA TGGCATTGCC CAGTGAGCAT
2101 GGACTTGAGC AGCCATCTCA CACCCCTCCC CAGACTCCAA CGCCCCCCAG
2151 TACTCCGCCC CTAGGAAAAC AGAACCCCAG TCTGCCAGCT CCTCAGACCC
2201 TGGCAGGGGG TAACCCTGAA ACTGCACAGC CACATGCTGG AACCTTACCG
2251 AGACCGAGAC CAGTACCAAA GCCAAGGAAC CGGCCCAGCG TGCCCCCACC
2301 CCCCCAACCT CCTGGTGTCC ACTCAGCTGG GGACAGCAGC CTCACCAACA
2351 CAGCACCAAC AGCTTCCAAG ATAGTAACAG ACTCCAATTC CAGGGTTTCA
2401 GAACCGCATC GCAGCATCTT TCCTGAAATG CACTCAGACT CAGCCAGCAA
2451 AGACGTGCCT GGCCGCATCC TGCTGGATAT AGACAATGAT ACCGAGAGCA
2501 CTGCCCTGTG AAGAAAGCCC TTTCCCAGCC CTCCACCACT TCCACCCTGG
2551 CGAGTGGAGC AGGGGCAGGC GAACCTCTTT CTTTGCAGAC CGAACAGTGA
2601 AAAGCTTTCA GTGGAGGACA AAGGAGGGCC TCACTGTGCG GGACCTGGCC
2651 TTCTGCACGG CCCAAGGAGA ACCTGGAGGC CACCACTAAA GCTGAATGAC
2701 CTGTGTCTTG AAGAAGTTGG CTTTCTTTAC ATGGGAAGGA AATCATGCCA
2751 AAAAAATCCA AAACAAAGAA GTACCTGGAG TGGAGAGAGT ATTCCTGCTG
2801 AAACGCGCAT AGGAAGCTTT TGTCCCTGCT GTTAATGCGG GCAGCACCTA
2851 CAGCAACTTG GAATGAGTAA GAAGCAGTGC GTTAACTATC TATTTAATAA
2901 AATGCGCTCA TTATGCAAGT CGCCTACTCT CTGCTACCTG GACGTTCATT
2951 CTTATGTATT AGGAGGGAGG CTGCGCTCCT TCAGACTTGC TGCAGAATCA
3001 TTTTGTATCA TGTATGGTCT GTGTCTCCCC AGTCCCCTCA GAACCATGCC
3051 CATGGATGGT GACTGCTGGC TCTGTCACCT CATCAAACTG GATGTGACCC
3101 ATGCCGCCTC GTTGGATTGT CGGAATGTAG ACAGAAATGT ACTGTTCTTT
```

FIGURE 1, page 1 of 2

3151 TTTTTTTTTT TAAACAATGT AATTGCTACT TGATAAGGAC CGAACATTAT
3201 TCTAGTTTCA TGTTTAATTT GAATTAAATA TATTCTGTGG TTTATATG

FEATURES:

5'UTR:	1-99
Start Codon:	100
Stop Codon:	2509
3'UTR:	2512

Homologous proteins:

Top 10 BLAST Hits

	Score	E
CRA|147000022595308 /altid=gi|10435148 /def=dbj|BAB14506.1| (AK...	1500	0.0
CRA|335001098671246 /altid=gi|11560044 /def=ref|NP_071580.1| na...	1331	0.0
CRA|18000005158484 /altid=gi|7662242 /def=ref|NP_055674.1| KIAA...	645	0.0
CRA|335001098684832 /altid=gi|11425473 /def=ref|XP_008288.1| KI...	645	0.0
CRA|335001098688185 /altid=gi|11431577 /def=ref|XP_007992.1| hy...	452	e-126
CRA|335001098646266 /altid=gi|11545733 /def=ref|NP_061830.1| SH...	421	e-116
CRA|18000004990129 /altid=gi|6677931 /def=ref|NP_033190.1| SH3-...	390	e-107
CRA|89000000202138 /altid=gi|7300563 /def=gb|AAF55715.1| (AE003...	264	3e-69
CRA|66000019404309 /altid=gi|8922344 /def=ref|NP_060524.1| homo...	251	2e-65
CRA|18000005246399 /altid=gi|7512523 /def=pir||T12533 hypotheti...	190	4e-47

EST:

gi|10993873 /dataset=dbest /taxon=96...	1524	0.0
gi|11003732 /dataset=dbest /taxon=96...	1495	0.0
gi|12040806 /dataset=dbest /taxon=96...	1170	0.0
gi|10948137 /dataset=dbest /taxon=96...	1049	0.0
gi|11303345 /dataset=dbest /taxon=96...	1043	0.0
gi|7933255 /dataset=dbest /taxon=960...	918	0.0
gi|10332226 /dataset=dbest /taxon=96...	912	0.0
gi|11643637 /dataset=dbest /taxon=96...	906	0.0
gi|10348166 /dataset=dbest /taxon=960...	664	0.0
gi|4753575 /dataset=dbest /taxon=9606 ...	609	e-171

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

Expression information from BLAST dbEST hits:

gi|10993873	Neuronal teratocarcinoma
gi|11003732	Umbilical vein endothelial cell
gi|12040806	Iris
gi|10948137	Teratocarcinoma
gi|11303345	Breast
gi|7933255	Leiomios
gi|10332226	Uterus
gi|11643637	Kidney renal carcinoma (ascites)
gi|10348166	Uterus leiomyosarcoma
gi|4753575	Human fetal heart

Expression information from PCR-based tissue screening panels:

Human leukocytes

FIGURE 1, page 2 of 2

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  1 MKKQFNRMKQ LANQTVGRAE KTEVLSEDLL QIERRLDTVR SICHHSHKRL
 51 VACFQGQHGT DAERRHKKLP LTALAQNMQE ASTQLEDSLL GKMLETCGDA
101 ENQLALELSQ HEVFVEKEIV DPLYGIAEVE IPNIQKQRKQ LARLVLDWDS
151 VRARWNQAHK SSGTNFQGLP SKIDTLKEEM DEAGNKVEQC KDQLAADMYN
201 FMAKEGEYGK FFVTLLEAQA DYHRKALAVL EKTLPEMRAH QDKWAEKPAF
251 GTPLAEHLKR SGREIALPIE ACVMLLLETG MKEEGLFRIG AGASKLKKLK
301 AALDCSTSHL DEFYSDPHAV AGALKSYLRE LPEPLMTFNL YEEWTQVASV
351 QDQDKKLQDL WRTCQKLPPQ NFVNFRYLIK FLAKLAQTSD VNKMTPSNIA
401 IVLGPNLLWA RNEGTLAEMA AATSVHVVAV IEPIIQHADW FFPEEVEFNV
451 SEAFVPLTTP SSNHSFHTGN DSDSGTLERK RPASMAVMEG DLVKKESPPK
501 PKDPVSAAVP APGRNNSQIA SGQNQPQAAA GSHQLSMGQP HNAAGPSPHT
551 LRRAVKKPAP APPKPGNPPP GHPGGQSSSG TSQHPPSLSP KPPTRSPSPP
601 TQHTGQPPGQ PSAPSQLSAP RRYSSSLSPI QAPNHPPPQP PTQATPLMHT
651 KPNSQGPPNP MALPSEHGLE QPSHTPPQTP TPPSTPPLGK QNPSLPAPQT
701 LAGGNPETAQ PHAGTLPRPR PVPKPRNRPS VPPPPQPPGV HSAGDSSLTN
751 TAPTASKIVT DSNSRVSEPH RSIFPEMHSD SASKDVPGRI LLDIDNDTES
801 TAL
```

FEATURES:
Functional domains and key regions:
[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

Number of matches: 6

1	13-16 NQTV
2	449-452 NVSE
3	463-466 NHSF
4	470-473 NDSD
5	515-518 NNSQ
6	796-799 NDTE

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 2

1	494-497 KKES
2	621-624 RRYS

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 7

1	38-40 TVR
2	46-48 SHK
3	150-152 SVR
4	175-177 TLK
5	261-263 SGR
6	550-552 TLR
7	589-591 SPK

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 14

1	60-63	TDAE
2	83-86	TQLE
3	96-99	TCGD
4	109-112	SQHE
5	171-174	SKID
6	175-178	TLKE
7	214-217	TLLE
8	233-236	TLPE
9	261-264	SGRE
10	308-311	SHLD
11	349-352	SVQD
12	415-418	TLAE
13	468-471	TGND
14	742-745	SAGD

[5] PDOC00007 PS00007 TYR_PHOSPHO_SITE
Tyrosine kinase phosphorylation site

117-124 KEIVDPLY

[6] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 10

1	56-61	GQHGTD
2	251-256	GTPLAE
3	290-295	GAGASK
4	322-327	GALKSY
5	538-543	GQPHNA
6	574-579	GGQSSS
7	575-580	GQSSSG
8	605-610	GQPPGQ
9	704-709	GNPETA
10	739-744	GVHSAG

[7] PDOC00161 PS00178 AA_TRNA_LIGASE_I
Aminoacyl-transfer RNA synthetases class-I signature

706-716 PETAQPHAGTL

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	415	435	0.842	Putative

BLAST Alignment to Top Hit:

>CRA|147000022595308 /altid=gi|10435148 /def=dbj|BAB14506.1|
(AK023281) unnamed protein product [Homo sapiens]
/org=Homo sapiens /taxon=9606 /dataset=nraa /length=726
Length = 726

Score = 1500 bits (3840), Expect = 0.0
Identities = 726/726 (100%), Positives = 726/726 (100%)

```
Query: 78  MQEASTQLEDSLLGKMLETCGDAENQLALELSQHEVFVEKEIVDPLYGIAEVEIPNIQKQ 137
           MQEASTQLEDSLLGKMLETCGDAENQLALELSQHEVFVEKEIVDPLYGIAEVEIPNIQKQ
Sbjct: 1   MQEASTQLEDSLLGKMLETCGDAENQLALELSQHEVFVEKEIVDPLYGIAEVEIPNIQKQ 60

Query: 138 RKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEMDEAGNKVEQCKDQLAAD 197
           RKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEMDEAGNKVEQCKDQLAAD
Sbjct: 61  RKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEMDEAGNKVEQCKDQLAAD 120

Query: 198 MYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEKTLPEMRAHQDKWAEKPAFGTPLAEH 257
           MYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEKTLPEMRAHQDKWAEKPAFGTPLAEH
Sbjct: 121 MYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEKTLPEMRAHQDKWAEKPAFGTPLAEH 180

Query: 258 LKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLKAALDCSTSHLDEFYSDP 317
           LKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLKAALDCSTSHLDEFYSDP
Sbjct: 181 LKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLKAALDCSTSHLDEFYSDP 240

Query: 318 HAVAGALKSYLRELPEPLMTFNLYEEWTQVASVQDQDKKLQDLWRTCQKLPPQNFVNFRY 377
           HAVAGALKSYLRELPEPLMTFNLYEEWTQVASVQDQDKKLQDLWRTCQKLPPQNFVNFRY
Sbjct: 241 HAVAGALKSYLRELPEPLMTFNLYEEWTQVASVQDQDKKLQDLWRTCQKLPPQNFVNFRY 300

Query: 378 LIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWARNEGTLAEMAAATSVHVVAVIEPIIQH 437
           LIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWARNEGTLAEMAAATSVHVVAVIEPIIQH
Sbjct: 301 LIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWARNEGTLAEMAAATSVHVVAVIEPIIQH 360

Query: 438 ADWFFPEEVEFNVSEAFVPLTTPSSNHSFHTGNDSDSGTLERKRPASMAVMEGDLVKKES 497
           ADWFFPEEVEFNVSEAFVPLTTPSSNHSFHTGNDSDSGTLERKRPASMAVMEGDLVKKES
Sbjct: 361 ADWFFPEEVEFNVSEAFVPLTTPSSNHSFHTGNDSDSGTLERKRPASMAVMEGDLVKKES 420

Query: 498 PPKPKDPVSAAVPAPGRNNSQIASGQNQPQAAAGSHQLSMGQPHNAAGPSPHTLRRAVKK 557
           PPKPKDPVSAAVPAPGRNNSQIASGQNQPQAAAGSHQLSMGQPHNAAGPSPHTLRRAVKK
Sbjct: 421 PPKPKDPVSAAVPAPGRNNSQIASGQNQPQAAAGSHQLSMGQPHNAAGPSPHTLRRAVKK 480

Query: 558 PAPAPPKPGNPPPGHPGGQSSSGTSQHPPSLSPKPPTRSPSPPTQHTGQPPGQPSAPSQL 617
           PAPAPPKPGNPPPGHPGGQSSSGTSQHPPSLSPKPPTRSPSPPTQHTGQPPGQPSAPSQL
Sbjct: 481 PAPAPPKPGNPPPGHPGGQSSSGTSQHPPSLSPKPPTRSPSPPTQHTGQPPGQPSAPSQL 540

Query: 618 SAPRRYSSSLSPIQAPNHPPPQPPTQATPLMHTKPNSQGPPNPMALPSEHGLEQPSHTPP 677
           SAPRRYSSSLSPIQAPNHPPPQPPTQATPLMHTKPNSQGPPNPMALPSEHGLEQPSHTPP
Sbjct: 541 SAPRRYSSSLSPIQAPNHPPPQPPTQATPLMHTKPNSQGPPNPMALPSEHGLEQPSHTPP 600

Query: 678 QTPTPPSTPPLGKQNPSLPAPQTLAGGNPETAQPHAGTLPRPRPVPKPRNRPSVPPPPQP 737
           QTPTPPSTPPLGKQNPSLPAPQTLAGGNPETAQPHAGTLPRPRPVPKPRNRPSVPPPPQP
Sbjct: 601 QTPTPPSTPPLGKQNPSLPAPQTLAGGNPETAQPHAGTLPRPRPVPKPRNRPSVPPPPQP 660

Query: 738 PGVHSAGDSSLTNTAPTASKIVTDSNSRVSEPHRSIFPEMHSDSASKDVPGRILLDIDND 797
           PGVHSAGDSSLTNTAPTASKIVTDSNSRVSEPHRSIFPEMHSDSASKDVPGRILLDIDND
Sbjct: 661 PGVHSAGDSSLTNTAPTASKIVTDSNSRVSEPHRSIFPEMHSDSASKDVPGRILLDIDND 720

Query: 798 TESTAL 803
           TESTAL
Sbjct: 721 TESTAL 726
```

>CRA|335001098671246 /altid=gi|11560044 /def=ref|NP_071580.1|

nadrin; neuron-specific GTPase activating protein
[Rattus norvegicus] /org=Rattus norvegicus /taxon=10116
/dataset=nraa /length=780
Length = 780

Score = 1331 bits (3406), Expect = 0.0
Identities = 676/816 (82%), Positives = 697/816 (84%), Gaps = 49/816 (6%)

```
Query: 1   MKKQFNRMKQLANQTVGRAEKTEVLSEDLLQIERRLDTVRSICHHSHKRLVACFQGQHGT 60
           MKKQFNRMKQLANQTVGRAEKTEVLSEDLLQIERRLDTVRS+CHHSHKRL+ACFQGQHGT
Sbjct: 1   MKKQFNRMKQLANQTVGRAEKTEVLSEDLLQIERRLDTVRSMCHHSHKRLIACFQGQHGT 60

Query: 61  DAERRHKKLPLTALAQNMQEASTQLEDSLLGKMLETCGDAENQLALELSQHEVFVEKEIV 120
           DAERRHKKLPLTALAQNMQEAS QLE+SLLGKMLETCGDAENQLA ELSQHEVFVEKEI+
Sbjct: 61  DAERRHKKLPLTALAQNMQEASAQLEESLLGKMLETCGDAENQLAFELSQHEVFVEKEIM 120

Query: 121 DPLYGIAEVEIPNIQKQRKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEM 180
           DPLYGIAEVEIPNIQKQRKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEM
Sbjct: 121 DPLYGIAEVEIPNIQKQRKQLARLVLDWDSVRARWNQAHKSSGTNFQGLPSKIDTLKEEM 180

Query: 181 DEAGNKVEQCKDQLAADMYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEKTLPEMRAH 240
           DEAGNKVEQCKDQLAADMYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEK LPEMRAH
Sbjct: 181 DEAGNKVEQCKDQLAADMYNFMAKEGEYGKFFVTLLEAQADYHRKALAVLEKALPEMRAH 240

Query: 241 QDKWAEKPAFGTPLAEHLKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLK 300
           QDKWAEKPAFGTPL EHLKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLK
Sbjct: 241 QDKWAEKPAFGTPLEEHLKRSGREIALPIEACVMLLLETGMKEEGLFRIGAGASKLKKLK 300

Query: 301 AALDCSTSHLDEFYSDPHAVAGALKSYLRELPEPLMTFNLYEEWTQVASVQDQDKKLQDL 360
           AALDCSTSHLDEFYSDPHAVAGALKSYLRELPEPLMTF+LYEEWTQVASVQDQDKKLQ L
Sbjct: 301 AALDCSTSHLDEFYSDPHAVAGALKSYLRELPEPLMTFSLYEEWTQVASVQDQDKKLQYL 360

Query: 361 WRTCQKLPPQNFVNFRYLIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWARNEGTLAEMA 420
           W TCQKLPPQNFVNFRYLIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWA+ EGTLAE+A
Sbjct: 361 WTTCQKLPPQNFVNFRYLIKFLAKLAQTSDVNKMTPSNIAIVLGPNLLWAKQEGTLAEIA 420

Query: 421 AATSVHVVAVIEPIIQHADWFFPEEVEFNVSEAFVPLTTPSSNHSFHTGNDSDSGTLERK 480
           AATSVHVVAVIEPIIQHADWFFP EVEFNVSEAFVPL TP+SNHS HTGNDSDSGTLERK
Sbjct: 421 AATSVHVVAVIEPIIQHADWFFPGEVEFNVSEAFVPLATPNSNHSSHTGNDSDSGTLERK 480

Query: 481 RPASMAVMEGDLVKKESPPKPKDPVSAAVPAPGRNNSQIASGQNQPQAAAGSHQLSMGQP 540
           RPASMAVMEGDLVKKESPPKPKD VSAA P  GRN++QI +  NQ Q    SHQLS+G
Sbjct: 481 RPASMAVMEGDLVKKESPPKPKDSVSAAAPVAGRNSNQITTVPNQAQTGGNSHQLSVGTA 540

Query: 541 HNAAGPSPHTLRRAVKKPAPAPPKPGNPPPGHPGGQSSSGTSQHPPSLSPKPPTRSPSPP 600
           H+AAGPSPHTLRRAVKKPAPAPPKPGNPPPGHPGGQSS GT       SPKP TRSPSPP
Sbjct: 541 HSAAGPSPHTLRRAVKKPAPAPPKPGNPPPGHPGGQSSPGT-----GTSPKPSTRSPSPP 595

Query: 601 -------------TQHTGQPPGQPSAPSQLSAPRRYSSSLSPIQAPNHPPPQPPTQATPL 647
                        Q   Q   Q     Q    RR SSSL PIQAPNHPPPQPPTQ
Sbjct: 596 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQTPGMRRCSSSLPPIQAPNHPPPQPPTQ---- 651

Query: 648 MHTKPNSQGPPNPMALPSEHGLEQPSHTPPQTPTPPSTPPLGKQNPSLPAPQTLAGGNPE 707
              +   QGP             +P  TPPQTPTPPSTPP  KQN S           E
Sbjct: 652 --PRLGEQGP-------------EPGPTPPQTPTPPSTPPPAKQNSS----------QSE 686

Query: 708 TAQPHAGTLPRPRPVPKPRNRPSVPPPPQPPGVHSAGDSSLTNTAPTASKIVTDSNSRVS 767
           T Q H GTLPRPRPVPKPRNRPSVPPPP PPG H  GD  LT + PTAS+IVTD+NSRVS
Sbjct: 687 TTQLH-GTLPRPRPVPKPRNRPSVPPPPNPPGTH-MGDGGLTPSVPTASRIVTDTNSRVS 744

Query: 768 EPHRSIFPEMHSDSASKDVPGRILLDIDNDTESTAL 803
           E  R+IFPE+HSD ASK+VPG ILLDIDNDTESTAL
Sbjct: 745 ESLRNIFPEIHSDLASKEVPGHILLDIDNDTESTAL 780
```

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF00620	RhoGAP domain	191.2	1.6e-53	1

Parsed for domains:

Model	Domain	seq-f	seq-t		hmm-f	hmm-t		score	E-value
PF00620	1/1	266	415	..	1	170	[]	191.2	1.6e-53

FIGURE 2, page 5 of 5

1 CTCGTGGCTG AGTTTAATTA CACACTCTTG CTCTAGCTGT AAGGCAGAGC
51 TCTCCAGGTT AGCTTCAGTG GACAATCTTT TCATGGTTTT CTCAGAGTTG
101 TTTCTTCCAA TAGCCTCTTT TCAGCTAGGG GTCTCACTCT GTCACCCAGA
151 CAAGAGTGCA ATGGTGTGAT AATAGCTCAC TGCAGCCTCA AATTCCTGGG
201 CTCAAATGAT CCTGTTGCCT CAGCCTTTCA ACTAGTTGGG AGTACAGGTG
251 CATGCCACTG CTTCTGGCCT TTTTTTTTTT TTTAAATTTT TCATAGAGAT
301 GAGGTTTTAG TATGTTGTCC AGGCTAGTCT CATACTCCTG AGCTCAAGTG
351 ATCTTCCCAT CTTGACCTCC CAAAGTGCTA GGATTACAGG TGTGAGCCAC
401 TGCACCTGGC CCCAGAAGAT AATTTTTTAT TTGTCTTTTA CTCTATGTTC
451 AAATTCTTCA ATTTTTTGGT AGACTCTACT TTTTCAATTT GTAGAGCTTG
501 CATGAATAGT GTTTTCCTTC TCTTGAAGTT TAGAGAGATC ATGTACTGTA
551 ATTCCTGAGC CACCTTGCTG TAACAAATTT TCCAGTTCTT CAATCTTTTC
601 TTCCTAATTG CTTAGATTTT CTTGATGCTT ACAACTTATT TCCCTCAATT
651 TCTGTTGATG AACATTCTGT AATACTGATA ATTCAAGCTG ATGGTCATCA
701 GTATCCTGAC TTCTTTTTTG TTTGAGCTCC TTGATGATAT TAATATTTGG
751 TGTTTGTAGT TTGTAGATTT CATTTTCATC AAAACTAGTT GTTCCTCCTA
801 TTTTATAAGT CTGAGCAATA CATTTCCAAT GGCCAACTGG AGACTCAAGT
851 TTTAGAACTT CATTGGACTA TCTGTTTATT TCTTGTTATG ATGAAATTAT
901 GTCATAAAAA CCCATGTAAG CGTCGTGGAA CACTGAAGCA TGATGGGTAC
951 CACATGGAAT GGAGGGGATG CAGTGTGGAT GGGAACCTCC GGCCTTCCCT
1001 GAATGTGCTG ACTCCAGGGC TGGCTGCCGG TCCTGCAACC GATCCTGTAG
1051 TGCTTGCTTT CTTGTTTTAG GAAGGCTCAT TTCTACCTCT TTCTGTTGTA
1101 ATTGATGTCG ATAACTTTTA GTTTGCTGCC CTATCTGAAG CTCTGATGCT
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15451 AGACAGGGTT TCGCTTTGGT CAGATTGGTC TTGAACTCCT GACCTCAGGT
15501 GATCCTCCTA CCTTGGTCTC CCAAAGTGCT GGGATTGCAG GCATGAGCCA
15551 CTGCACCTAG CCTGCATCAG TATGGTTTAA TAACTGTTGA TCTGTAATAT
15601 GTTTTAAATT GGGTAGAGCT GGTCTCTTAC AAATACTCTT TTTCAGGCTG
15651 GGTTTGTGGC TCACGCCTGT AATCCCCAGC ACTTTGGAAA GCTGAGGCCG
15701 GAGGATCGCT TGAGGCCAGG AGTTCAAGGC TGCAGTGAGC TGTGGTCCTG

FIGURE 3, page 5 of 33

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16051 ATGACTTTGT GTGTACAATC TTTTATATGC TTCCCAGGTA TTTTTTTTTG
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16551 ATATGGAGAA AACAATTGCA ATGCACTTTA GATTTAGGAA CAAATTGGAG
16601 GAGAAAGTTG AGAAATGGTA AGAGGAGTTT TAATGGAGCG TATGTGGCAG
16651 TATGCTAATG TCACTTCTAA AGAAGAGGTG GTTAGCAGGT CACAAGGCAG
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16951 GTTACAGTTC CCATGCTGGG AGCTGCTCTC TAGAGAAATG TTATTTGCAG
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17301 CTGTGACCTT GGTCCAATCA GCCACTCTGC TGTGTTCCTA TACGTGAGAA
17351 ACGGCTCCTG ATACCACCAG GAGCAAGCTC TGCTGTGTTT AAGAAGGTGG
17401 TGTGTGCTAG GGAGGCGTCA TGAGACAGTG AGGACATACA GTGTGACACA
17451 GCAGGTCAGC ACTGGGGAAA ATAGCCAGGT TAGCCTTCAC TTCACTGCTC
17501 TATGCCAAAA TACATTCCAA ATGGGTTAAA GCTTTCATGT AAAAAATAAA
17551 ACCACAAAAT AAATACAAGA AAATATAGCT TATTGTGGAA AGTACTGCAT
17601 GCTTTGGCAT AAAAATGTGG AGAAAGAACA ATAAAAGATA GCCTGTAGGT
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18851 TAATTTCCTA AGAAAACTGG ACATGGCCAC CTTTCCCCAG TGTCTGAGGC
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19251 CCGCACCTCG CTCCTGGCTT CTTCCCTGCC CTCCCTGGGG ACTCCTATCC
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23051 GCTTTTTTGA CAAAACACCT CATTAAAAAG CAATCAGATT TCTGTTTTAA
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23501 ATATAAATAA AGTAAGGGGC AGAAAGGTTA AGGGATGTAT TTTTAGATGC
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86401 AATGTGCCAA GGTTTCCATT AACCCAAAGG GTGACGGTTA ACTGATTCTA
86451 ACAGCTTTTG ATAACTTTTT TCAGGAATAT AATACATAAT TTGCACATGT
86501 TATAAATGGT TAATAACTTT TTTTCTGATG CCATCAGAGC TTTTATTTTG
86551 AAAACAACAA AGCCATGTTG GTTTGTTTGT TTTGTTTCCC AATAGATGCC
86601 CTTCCTAGTG CCCTCACAGG TGGGGAAGGT TTCCAGGACT AAGGTCTGTA
86651 ATGGCCCCGA GCAGCTTGCC CCATAGCTCG CCCCACAGCT CCAAATGCTC
86701 CTGCTTAGCC GTGTTTTGCA TATGTGCTTT TGACCATGTG CTCAGGAGCA
86751 GCCGTTTGAC CGTGTGCCCT GACAGCCAAT AGGCCATCCA TTCTGTAGCA
86801 TATTGACATT TCTTTATTTT TATCAGAAGC ACTTTGAGCT GCAGTGCTTC
86851 AAATTCGAGG AGTAGATGTC AGTAGATCAA GAGCCTGATT TCAAGCTGCT
86901 CTTGAAGAGT ATCTTCTTTC TTAGGGGCCA AGCACAGTGG CTCGTGCCTC
86951 TAATCCCAGT ACTTTGAGTG GCTGAGGCAA GAGGATTGCT TGAGCTCAGG
87001 AGTTCGAGAC TGCAGTGGGT AGTGATTGTG TCACTGCACA CTGCAGTCCA
87051 GCCTGCATGA CAGAGTGAGA CCCTGCCTCT TTTTAAAAAA AAAAAAAAAA
87101 AGGAATATCT TCTATCTTTT TGGTGAGCCT CTTAGCAGCA GTCTACTCTT
87151 CCCAGTGTGA TTTACCTGTC ACTGATGGGC TCACCAGCAT CCAACCAAAG
87201 AGGACCCAGG TGCAGTCAGC ACGGGAGGAA ATTGTGTCCT TTGTGTCTTG
87251 AGCTTTAATT TTAAATTTTT GTATTTTAAG TGCAAGTTAA CTGCATGGAG
87301 CTTCTTAATT TGATATTTTA AATTCTCAAG ACCAAAAAAT TAAAAAAAAT
87351 CTTCCGCCAA ATACCCTACA CTGAATTATT TTAAATTCCT TTGCATCCTA
87401 GCATGCTTAC GTTTTGCTTT ATTAAACCAT ATGAGCTTTT TAAAAGGCAC
87451 TGTGAGCTCA TCTAAGTCTG CCGCTGGGTC TACATGTGGA CAGCATAAGG
87501 CCCTCATCAT ATGTACAGCT GCTTTAATCA GCTGGCCTGA GCCTTAGGCC
87551 TACTGTGGGC CCCTTAGCCA GAGTGCTCAC AGCTTAGGTC TGAGTAAGAC
87601 TTTCTGTAGG AACCGTAAGT GGAAAACCAG AGTGTAGCCT TCAAAACAGG
87651 GAGGAGGCCC GGGTGCGATT CCACAATTTC ATGCTTGTGA CACACCAAAA
87701 TGTTATTATC AGATATTTCC TTTTATTTAA ATGAAAGATT GCAAACCAGA
87751 ATTATGCCTA TTTTTTAATA CCATTGTTAC CCGGGGTGTA TTTATTCCAC
87801 AAGTTTAGTT TACTGATCTG CTACAACACT GTAATATACT GCCTGTAATT
87851 ATTAGATAAG TGAAATTTTA CATTAAAAAT GTGTTTCCCG AAGATACTAG
87901 CTATTTAAAA ACCGGTCTAT GCTATGAATT CTCCTAACTC AAGAAATTCC
87951 AGGTTACCAG AGTTATCTTT GTATTACAGA ATTAACCTGT ACTATCTTAA
88001 AATCCCCTGG CCTCCCACTG AAAGTACACA GAAGGCCAAC ATTTAGAATT
88051 TTTTAATCTG CTAGTATTGA TCATACTGCT ATTAACCATT CTTGGATGTA
88101 GCCATTGGGT TTTTCAAGGA GGAAAAAATA TATAACTTCC TTGGACAGGA
88151 TGGTCCTTTA TTATGACATA ATGTTTTCAC TTAGAAAACT TTAGATGGAC

88201 AAATTCCTGA AAACAGGTTA TTCCTTTAGA ATTGGATTAA GTTAGAGTTT
88251 TAAAGAGTTG GGTTAAGGCT AATGGGATTA AGATAAACTC TTGGGGGGAG
88301 ATTATTGCTG CCAAGCAGGT TTGGCAGCCA ACTTCTCACA GCTCAGCACC
88351 AGCACTGGAG GATGCCGGCA TTCTGGCATC ATTTTGAGTC TCCTGTTAAT
88401 TGTGACTCTA GAGAGCAGTA AGAGTTTTAA TTCCCATGTA AAAGAGTTTA
88451 CATCTTGCTA TTTTTGAAGT AATAGATTTT AGCAAAGAGT ATTCTAATTT
88501 AAACATTTTA TTAAATAATT TAGATGTATG ACCTGCCATA TTCAGTAAGA
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88601 GCATTTTTGC TACTTGATGA TCATATTTGT GCACTCATGC CTGTTACTAA
88651 CTGGCCACCC TAACCCTGCC TGCTTGCATC CCTACTAATA GTGCATGCAC
88701 TGAAGGAGGA CTGGCTTTGT TGATGCTTGC TGCAATGATT CGGAATACTA
88751 AGTGTGTACC CAGATGTGGA ACAGGTGGTC ACAGGGCTGT CCTTGTTACT
88801 TCTTTAATTT CCATTCTTTT CCATATCAGG CAAGCTTGAG GTATAGTAGG
88851 AAGAACACAC ATTATGGAGT CAGACCTGAC TGAGTTAGAA TTTCAGCTCT
88901 TGGTATAACA TAGGCTAGGC ACAACCTGGC TGATCTGTAA AGTGGTGACA
88951 TCTGTCTAAA TTGTTGAAGA TGAAATAAGA GAAAGTCCAA GATTATTCTG
89001 TTAGCCAGTT ACAGTTCTTA ATATACGCGC AATCTCGGCT CACTGCAAGC
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89101 GGGATTATAG GCGCCTGCCA CCACATCTGG CTATTTTTTT TATTTTTAGT
89151 AGAGACGGGG CTTCACCATG TTGGCCAGGC TGGTCTCGAA CTCCTGACCT
89201 TAGGTGATCC GGCCTCCTCA GCCTCCCAAA GTGCTGGGAT TATAGGTGTG
89251 AGCCATTGTG CCTGGCCTGC TATTTATCAT TTTTATCTAG AAGAAAATAG
89301 TTTTAATCAG ATTTCTATGT TAGATTCACA TATCAGGGTT TTAAAAACTC
89351 ATACGCCCGG ACCCGGCCTT CTAGGACCCA AACACAGGAG ACTGGGGGTG
89401 GAACCCAGGT ATCCATATTT TGATTCTGAT GCACCACTTG GTTTTTTGAA
89451 TCTCACTTCT TTCATGGGTT AAAAAGACAA TGCTCTGCAG AAGGAGATAA
89501 CATATACATT CATATAATTT AGTGAGCCTG AGACTGTCTG TGAGGCGTTA
89551 GTCCACTGTA CCACAGATAG ACCAAATCAC TCACAAAGTA GCCATAAGCC
89601 TGGACACTTT GCTGGCTAAT TTCATAGTGT TTGCTTTTTA AACTCTCACC
89651 CTTCTTATGT CATGTAAGTA ATGCCTTTTT AAAAATAAGC ATGAGCTGGG
89701 GCACGGTGGC TCACGCCTGT AATCCCAGCA CTTTGGGAGG CTGAGGCGGG
89751 TGGATCACTT GAGGTCAGGA GTTCAAGACC AGCCTGGCCA ACATGGGGAA
89801 ACCCCATCTC TACTGAAAAT ACAAAAAGTT AGCTGGGTGT CGTGGTGGGT
89851 GCCTGTAATC CCAGCTACTT GGGGAGGCCA AGGCAGGAGA ACTGCTTGAA
89901 CCCAGGAGGT GGAGGTCGCA GTGAGCTGAG ATCGTGCCAC TACACTCCAG
89951 CCTGGGTGAC AGAGTGAGAC TCTGTCTCAA ATAAATAAAA ATAAGCATGG
90001 ATATTAAAAC TCTTGAGAAA TGGAAATAAT AAGAAATCAA CTGTAGCTAT
90051 ACAATTGAAA AAGTCTGCCA TTTATATTCT ACTTTTTTTC TTTTCTCCTC
90101 TTCTCTTCTC TTCTCTTCTC TTTTCTTTTC TTTTCTTTTT TTTTTTCAG
90151 ACGGAGTCTC ACTCTGTTCC CCAGGCTGGA GTGCAGTGGC ACGATCTTGG
90201 CTCACTGCAA GCTCCGCCTC CTGGGTTCAC ACCATTCTTC TGCCTCAGCC
90251 TCCCGAGTAG CTGGGACTAC AGGCGCCCAC CACCACGCCC AGCTAATTTT
90301 TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTAGCCA AGATGGTCTC
90351 GATCTGCTGA CCTTGTGATC TGCCCGTCTC GGCCTCCCAA AGTGCTGGGA
90401 TTACAGGCGT GAGCCACCAC ACCCGCCCCT TTTTTTCTTT TAGTTTTTCT
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90501 ATCCTTTTAT TTCACTTTAC ATCATATGCT CGTTCTCATG TGATAATGTA
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90601 TGTATTATTA CTCCTAGTTG GATATTTAAG TGGCTTCTGT TTCTACTTGC
90651 AGTTTATTTT TAATAAGTAG ATAATCAGAA TTGTGTCAAG ATAACATCCA
90701 GTGAGACTTG AACAGAATCA CTCCTGAATA GTTGACTCAG AGTCTCTAAT
90751 AGCCCTAGAA AACTGACGAG AAATCATCAG TTCCTGATAA AATTACACAA
90801 TTCTACTTCA ACCAAAGAGG ATCAAAGCCA GATTGGTTGG ACTGTCATTC
90851 TTCTGTTTAT TTATTTTGTG TATTTTTTGA GACAGAGTCT TGCTCTGTCA
90901 CCCAGGCTGG AGTGCAGTGG TGCAATCTTG GCACACGGCA ACCCCTGCCT
90951 TCCTGGTTTA AGCAGTTCTC TTGCCTCAGC CTCCCAAGTA GCTGGGATTA
91001 TAGGCAGGTG TGGCAACACC TGGCTGATTT TTGTATTTTT AGTAGAGACA
91051 GGGTTTTGCC ATATTGGCCA GGCTGGTCTC CAACTCATGA CTTCAAGTGA
91101 TCCACTCACT TCTGCCTCCC AAAGTGCTAG GATTACAGGC ATGAGCCACC
91151 GCACCTGGCC CCATCATTCT TAATCACCCT AACATTTTCC CTCTTTCCCA
91201 AAAGAGTTGT GTATATCCTT GGGTGAGGAT CCTGAAAGTG AAGACATTAT
91251 CTGAGGAAAT AATGGTTTGG GTCTTAAACA CTCTGGTTAG AGCTAAGTTT
91301 ATATGACAGG TATTACATTG TAAAAAGGAG AAAAAGGTTA TTTTAGAAAG

91351 ACACCTGTTA GAACCTGCTT TTTTTTTTAT TTTTTTTTAT TTTTGAGACT
91401 GAGTCTTACC CCGTTGCTCA GAATGGAATG CAGTGGTGCG ATCTCAGCTC
91451 ACTGTGACCT CCACCTCCCA GGTTCAAGCG ATTCTCCTGC CTCAGCCTCC
91501 TGAGTAGCTG GGATTACAGG CACTCACTAC CGTGCTCGGC TAATTTTTGT
91551 ATTTTTAGTA TAGACGGGGT TTCACCATGT TGGCCAGGCT GGTCTTGAAC
91601 TCCTGACCTC AGGTGATCTG CCTGCCTCGG CCTCCCAAAG TGCTGGGATT
91651 ACAGGCATGA GCTACCACAC CCAGCCAGAA CCTGCTTTCT AAAAGCACCC
91701 TAAACCTCTT TGGTTGTGAA TTTATATATT CTCTGCCTTC CAAGGGCTGG
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91801 AAAAAAAAAA AAAACAGAAA AGAGACCTCC AATAAAAGGT TTCTTTTTTG
91851 TCTGATTTTT TGCTTTTTTT TAATTTTGAA ATATAATACT TGTCATATAA
91901 ACTTAGCTCC AAGCAGTATG CTCAAAGACC AGCCCTTCTT GGAATGCAAA
91951 TAATATATAA ATTCATAGCC AGAGACGTTT AGAGGTGTTT AAAGAAAACC
92001 AGGTTCTTAC AAGTGTCTTT CTAAAATAAC CTTTATCTCT TTTTTACAAC
92051 AATCAACCAG AGTGTTTAAG ACTCAAACCG TTCACTGGTG AAGGAAGGCA
92101 TTCCCTGAGA CTCTAGGTCT GAGAAGAGGG ATGGGTGGTG GAGAGGGGGA
92151 GGGAGTTTAT TCGCCCTGCA GTTGTGCCTG CACCACTTAC TTTCAAGGGC
92201 ATATTTGGAT CTGTTACTTG TCAAAGTGGC TATCAGAATC ACCTTGGACT
92251 TCTTGAAGGG TGAGTTCACA ACCGAGAAAG CACATATTCA AAATTGTTGA
92301 AGTAATAAGT AAATCTTCTA GAACCTTACC CTCAGTGATA ACATTCCACT
92351 TCTAGCTCTT AAATACCCAC TTCTGTTTCC TGGATGAGAT ACTCAGTGCA
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92451 TATCAAGTTC TGCCTTTGGG CTGAGGCTGG TTACTGGAGG TCATCCTCTG
92501 TTTCTCTCTT TTTTTTTTTT TTTTTTTTTA AAAAAAAGAG AGACAGGGTC
92551 TTGCTCTGTT GCCCAGGCTA GAGTGCAGCG GTGTGATTCC AGTCCACTGC
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92651 GAACTAGAGG CATGCACCAC CACACCCGGC TAATTTTTGT GTTTTTCTTA
92701 TAGAGACGGA GTCTCATGTT GCCCTGGGCT GGTCTCGAAC TTCTGGGCTC
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92801 TCTTTTGTAT GAACTTAGCT CCAAGCATAT GCTCAGAAAC CAGCCCTTCT
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92951 CTTTTTACAA CAAACCAGAG TGTTTGTAAG ACTGAAACAA TGATCTTGGA
93001 TAATGTCTTT GAAGGCCCTC ACCCAGGGAT TTACAGACTC CTCTGGGGAG
93051 GAGGGAAAAT GTAATGCGAA GAGCCAGAGT GCAACCAATC TGGCTTTGAT
93101 CCTCTTTGGT CCACACTGGC TGTGTCACCT TGGGCAAGGA ATAGAGCCTC
93151 TGAGTCTCCC TTTCTTATTT CTGCTGCCTT AGGATTAGTT AGTGGGGGTT
93201 CAGTGAGACG ATGTAATAAA GTGTGGGTGT ATAGTACAGT CTCTGGTGTA
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93301 ATGCTGGTAA TCCCAGCACT TTGGGGAGCC GAGGTGGGAG GATTGCTTGA
93351 GGCCAGGAGT TCAAGACCAG CCCAGTCAAC ATGGTGAAAC CTTGTCTCTA
93401 CCAAAAATAA AAAAAATTAG CCAGGCATGG TGGCGTATGC TTGTAGTCCT
93451 AGCTACTCGG GAGGCTGAGG TGGGAGGATC AGTTGAGCCC AGGAGGTGGA
93501 GGCTGCAGTG AGCTGAGATT GCACGACTGC ACTCCAGCCT GGGCAAAAGA
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93901 GGCTTGGTGG CTGATAGGCG TTAGCTTGCA TGTGAATACA GATATTAACA
93951 AGTAGAAATC TCATCCGTAT ACACAGTGCC TTTGCATCAT GCATTCCCCG
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94201 AGATGACTCT TCATGCATCC ATCCAACCAT CCAAGTGTGC AGCTACAAAA
94251 TTTCTTGAAC ATCTGCTATT TGCCGGTCAC TGTTTTAGGT ACTGAGGATA
94301 CACTGTGAAC AAGACAGACA CAGTCCCTGC CTTCGTTGAC TTCTGTTCTG
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94401 GGCTGCACCA TAGGCTGGTG CAGTTCTGCA CAGTGTCATT GGTTTTATAG
94451 TTATCACAAG ACCTGAATTG TCTGAAATGA CATTCAGCAC CTGAACTCTT

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94501 TGACACTTTG GCACCTCCAT AAATCTAGAA ATTTCTCTGA GTTGTGGTGC
94551 ATAGGAAACC TTGAGGGACA ACCCAGGAGT AACTGTGAGA AAAAGGGTGT
94601 CCCAGGGAGT AAATAGATCT CACAGCTCAG AACTGTAGGG ACAGGAAGGT
94651 GGAAGGGGTA GGAGCTGGAA CAAGTCTCCA AGCAGTGAGC TTCCCCAAAG
94701 TGCACCAGCG TTTTCAAGCT GTGCCTGCGT AGACGGGAGC AGGTCGAACA
94751 GAAATATAGT CAAAACTAGC TCCCGTCAAG GACAGACAGG ATGTCATTTT
94801 GCACCACAGC AAGTAGGGGA AAGCAGCTCT CAAGCCTAAC TGTGAAACGC
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94901 TACCTCTAAC GCAGCAAAGC AAAACTACAA AACATCTCTC TTCTCTCTTA
94951 CACCAGCCCT AAAATACCTA ATGAGGCTCT CATAATTTGC CAGAACCCAC
95001 ATCTACGAGA GAAGCCAGCC CTTTTGTCTT AATTAGGATC CCCTTGGTCT
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95551 AGGCCCAAAT GTTGCTGGTG CTGAGGGTGA GGTCCTAGTG TTAGTAACAG
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95701 GGCTTCCTTT CCTCCATCAA AGCAAGCAAA TCCTTTAAAA GCTGCATCTC
95751 CAAGGGCTGC TCCGGGCTCA TAGCAAGCAA CGTCGGAGCC CAGAGGCAAG
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95951 CGGGGGTTAC CCCTCATTGA TACCATGTCT CCTCGTGTTT TTGTCCAGAC
96001 TCCAATTCCA GGGTTTCAGA ACCGCATCGC AGCATCTTTC CTGAAATGCA
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96151 CCACCACTTC CACCCTGGCG AGTGGAGCAG GGGCAGGCGA ACCTCTTTCT
96201 TTGCAGACCG AACAGTGAAA AGCTTTCAGT GGAGGACAAA GGAGGGCCTC
96251 ACTGTGCGGG ACCTGGCCTT CTGCACGGCC CAAGGAGAAC CTGGAGGCCA
96301 CCACTAAAGC TGAATGACCT GTGTCTTGAA GAAGTTGGCT TTCTTTACAT
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96401 GAGAGAGTAT TCCTGCTGAA ACGCGCATAG GAAGCTTTTG TCCCTGCTGT
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96601 AGACTTGCTG CAGAATCATT TTGTATCATG TATGGTCTGT GTCTCCCCAG
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96701 TCAAACTGGA TGTGACCCAT GCCGCCTCGT TGGATTGTCG GAATGTAGAC
96751 AGAAATGTAC TGTTCTTTTT TTTTTTTTTA AACAATGTAA TTGCTACTTG
96801 ATAAGGACCG AACATTATTC TAGTTTCATG TTTAATTTGA ATTAAATATA
96851 TTCTGTGGTT TATATGAAAA CTTCATAATT CTTGGAGGTA AATTGTGGAG
96901 TGTGTGTGTG TGTGTGTGCA TGAGTGTGTG TGTGTTGCCA CTCAACCAGA
96951 TAGAATTGTG GCTGGGACAT CTTGGGGGAG AGGGTCTAAT TGTAGCTGTA
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97101 AAGGCTGCAC CCTTGGTCCT CCCAGTGCTG GCATCCCTTT CTTTCCATCT
97151 AGAGATACTC AGACTCCCGG GGGCAGCTCA CAGGAGTTCA GCCCCACCGG
97201 GTTGGTGCAT TCGTCAGCAG TTGTGAATTG CCATAGAGAG CCCTTTTTCC
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97301 CTCCCAGGAT TGAAATACTA GGGAAGAGCC GATGGGGAAT TGGAGCAAAG
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97451 TTGGCTGCCC TGAGCCTTCT ATTGATCGAG TTTGCTAGGT GTGTCAGTGT
97501 CTAAGTCACT GCCTAGAAGA CACTGGGCCT CTTTCCACTA CGAACTGACT
97551 TAAGCCTGAT TTAAAAAGGG GAACCACAGT TTCCTTTTGT TGTTTTTTTG
97601 AAACAGATCT CACTCTGTGG CCCAGGCTGG AGTGCAGTGG CACAATCATA

97651 ACTCACTGCA GCCTCCAAAC TCCTAGGCTC AAATGATCCT CCCAACTCAG
97701 CCTCCCAAGT AGCTGAGACT ACAGGTGCAT GGCAATACAC CCAACTAATT
97751 TTTAAATATT TTTTTTTCTA GAGACAGGGA TCTTGCTGTG TTGCCCAGGC
97801 TGGTCTTACA ATTCTGGCCT CACGCAATCC TCCCACTTCA GCCTCCGAAA
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97901 TTACTCAGTT TCCTATGCCC TCAAAGTACT CCCTATACTT ATTAATTACC
97951 TTCAAAATAT GCTCCTGTAA GCCCATTTGC TCCCATATCT TGAATTTTCA
98001 TTGGCTTAAG GCTCACTCTT CCCCTGTGCC ACCTGTGTAT TGTTAATTTT
98051 CTATACCCTC CTTTAGCCAC AGAACAAACC CTGCAGAGAA AGAATCCTCT
98101 GTGTGGGCTG ATGCTCCATG TTGAGCACCT TCTCCAGGCG CCTGGCTGTC
98151 CACGGTCAGG TGTCTCCATG GAGCCTCGGA GATGCTCCCA TCGTGATGCC
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98251 GCTGTTGGCA CCTGGGGATG AGAAACATCC ATGCTGACAT CCTGCCCAGC
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98401 AATCTTCCTA CCCTGACAGC TGCAAACTTC AAAACAATGA AAGTCATTTG
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98501 GGCAGATCAC TTGATGTCAG GAGTTCAAGA CCAGCCTGGT CAACATGGTG
98551 AGACCCCATG TCTACTAAAG ATACAAAAAA TTAACTTGGC ATCGTGGTGG
98601 GTGCCAGTAA TCCCAGCTAC TTAGGAGGCT GAGACAGGAT AATCACTTGA
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98751 AACCCAGAAC TGTCTAGGGT GGGATACATG GCTGAGCATC CCACCGGCAG
98801 GGCCAGGAGA GGCACCTGGA TCCTCTTTCC CGTTCTGTGG CCCGGGATTC
98851 CTTCTGCTGG AGGCG

FEATURES:

Start: 2100
Exon: 2100-2152
Intron: 2153-38363
Exon: 38364-38403
Intron: 38404-40049
Exon: 40050-40154
Intron: 40155-46788
Exon: 46789-46862
Intron: 46863-48596
Exon: 48597-48708
Intron: 48709-48941
Exon: 48942-49018
Intron: 49019-53062
Exon: 53063-53174
Intron: 53175-56271
Exon: 56272-56340
Intron: 56341-56498
Exon: 56499-56580
Intron: 56581-61520
Exon: 61521-61648
Intron: 61649-63208
Exon: 63209-63320
Intron: 63321-63880
Exon: 63881-63962
Intron: 63963-66766
Exon: 66767-66847
Intron: 66848-68655
Exon: 68656-68769
Intron: 68770-72389
Exon: 72390-72481
Intron: 72482-74107
Exon: 74108-74264

Intron:	74265-80615
Exon:	80616-80785
Intron:	80786-84851
Exon:	84852-85472
Intron:	85473-95998
Exon:	95999-96126
Stop:	96127

CHROMOSOME MAP POSITION:

Chromosome 16